



1  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Unknown  
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid  
(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic  
(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1573

(D) OTHER INFORMATION: Primer 5' for PCR amplification of the first 44 amino acids of the recombinant protein of Neisseria meningitidis P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
TTCCATGGTA GATAAAAGAA TGGCTTTAG

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

[illegible]

**(B) STRAIN: B:4:P1.15**

(A) LIBRARY: Genomic

(B) CLONE: P64K

(A) NAME/KEY: 1575

(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

TTTCTAGATC CAAAGTAATC AGGGGTATCG

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(2) INFORMATION FOR SEQ. ID NO: 4

**(i) SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 26 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A)DESCRIPTION: Synthetic oligonucleotide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B)CLONE: P64K

**(ix) FEATURE:**

(A) NAME/KEY: Primer 2192

(D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 120 amino acids of the

# C O N T E N T S

[illegible]

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Fragment amplified by PCR

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Fragment derived from the first 47 amino acids of the recombinant protein of Neisseria meningitidis P64K, containing a NcoI site at the position 3 to 8 and a XbaI site at the position 139 to 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCCATGGTA GATAAAAGAA TGGCTTTAGT TGAATTGAAA GTGCCCGACA  
TTGGCGGACA 60

CGAAAATGTA GATATTATCG CGGTTGAAGT AACGTGGGC GACACTATTG  
CTGTGGACGA 120

TACCCTGATT ACTTTGGATC TAGAAA  
146

(2) INFORMATION FOR SEQ. ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:



1. The first group of people who are interested in the study of the history of the United States are the people who are interested in the history of the United States.

—

(B) STRAIN: B:4:P1.15

(B) CLONE: P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :  
CTAGATTGA TATCAG

16

(D) TOPOLOGY: Unknown

(A)DESCRIPTION: Synthetic oligonucleotide

(iv) ANTI-SENSE: No

•

(B) STRAIN: B:4:P1.15.

(B) CLONE: P64K

(A) NAME/KEY: 1577

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: JY1

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation JY1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: RF

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala Thr  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues.

(B) TYPE: Amino acid.

(C) STRANDEDNESS: Unknown.  
(D) TOPOLOGY: Unknown.

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: MN

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation MN.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr  
1                      5                      10                      15

(2) INFORMATION FOR SEQ. ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: BRVA

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:✓

Arg Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr  
1 5 10 15

**(2) INFORMATION FOR SEQ. ID NO: 14:**

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: IIIB

(ix) **FEATURE:**

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation IIIB.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile  
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues.

(B) TYPE: Amino acid.

(C) STRANDEDNESS: Unknown.

(D) TOPOLOGY: Unknown.

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Consensus sequence of the central region of the loop V3 belonging to the protein gp120 obtained from different isolations of the VIH-1, position 7 within the multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly  
1                      5                      10                      15

(2) INFORMATION FOR SEQ. ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

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[illegible]



(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB4.

000740-04000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ala Pro Thr Ser Ser Ser Thr Ala Gln Thr Gln Leu Gln Leu Glu  
 1 5 10 15  
 His Leu Leu Leu Asp Leu Gln Ile Phe Leu Ser Arg Gly Ile Arg Ile  
 20 25 30  
 Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly Gly Gly Ala Arg Gln  
 35 40 45  
 Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr Thr Thr Ala Gly Gly  
 50 55 60  
 Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala  
 65 70 75 80  
 Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile His Ile Gly Pro Gly Arg  
 85 90 95  
 Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg Lys Arg Ile Thr Met  
 100 105 110  
 Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly Gly Gly Ala Ser Ile  
 115 120 125  
 Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile  
 130 135 140

(2) INFORMATION FOR SEQ. ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB9.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile  
 1 5 10 15





[illegible]

(i) **SEQUENCE CHARACTERISTICS:**

(B) TYPE: Nucleic acid

(D) TOPOLOGY: Unknown

(A)DESCRIPTION: Synthetic oligonucleotide

(iii) **HYPOTHETICAL: No**

(iv) ANTI-SENSE: No

(v) **FRAGMENT TYPE:** Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

**(ix) FEATURE:**

[illegible]

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## SEQUENCE LISTING

SEQUENCE IDENTIFICATION NO.: 1

SEQUENCE TYPE: amino acid

LENGTH: 47 amino acids

MOLECULE TYPE: protein fragment.

PROPERTIES: First 47 amino acids of the recombinant protein P64k of *N. meningitidis*.

MLDKRMALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLETD

44

SEQUENCE IDENTIFICATION NO.: 2

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 5' No. 1573 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTCCATGGTAGATAAAAGAATGGCTTTAG

29

SEQUENCE IDENTIFICATION NO.: 3

SEQUENCE TYPE: Nucleotide

LENGTH: 29 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 1575 for PCR amplification of the first 44 amino acids from the P64k antigen of *N. meningitidis*.

TTTCTAGATCCAAAGTAATCAGGGTATCG

29

SEQUENCE IDENTIFICATION NO.: 4

SEQUENCE TYPE: Nucleotide

LENGTH: 26 bases

MOLECULE TYPE: Synthetic oligonucleotide

PROPERTIES: Primer 3' No. 2192 for PCR amplification of the first 120 amino acids from the P64k antigen of *N. meningitidis*.

GGCGGTTCTGCCGATTAAGGATCCGA

26

SEQUENCE IDENTIFICATION NO.: 5

SEQUENCE TYPE: Nucleotide

LENGTH: 146 base pairs

MOLECULE TYPE: PCR amplified fragment

PROPERTIES: Derived fragment from the first 47 amino acids of the P64k antigen of *N. meningitidis*. Restriction sites NcoI (positions 3 to 8) and XbaI (positions 139 to 144) are introduced by PCR, which provoke changes in the nucleotide sequence of this fragment.

TTCCATGGTAGATAAAAGAATGGCTTTAGTTGAATTGAAAGTGCCCGACATTGGCGGACA 60  
CGAAAATGTAGATATTATCGCGGTTGAAGTAAACGTGGGCGACACTATTGCTGTGGACGA 120  
TACCCTGATTACTTTGGATCTAGAAA 146

SEQUENCE IDENTIFICATION NO.: 6

SEQUENCE TYPE: amino acid

LENGTH: 47 amino acids

MOLECULE TYPE: stabiliser fragment derived from the first 47 amino acids of the P64k antigen of *N. meningitidis*.

PROPERTIES: This fragment has the following changes with respect to the P64k.  
L2→V2; E45→D45; T46→L46; D47→E47

MVDKRMALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLDLE 47

SEQUENCE IDENTIFICATION NO.: 7

SEQUENCE TYPE: Nucleotide

LENGTH: 16 bases

MOLECULE TYPE: Synthetic oligonucleotide

CTAGATTTGATATCAG 16

SEQUENCE IDENTIFICATION NO.: 8

SEQUENCE TYPE: Nucleotide

LENGTH: 16 bases

MOLECULE TYPE: Synthetic oligonucleotide

GATCCTGATATCAAAT 16

SEQUENCE IDENTIFICATION NO.: 9

SEQUENCE TYPE: amino acid

LENGTH: 15 amino acids

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1. LR150 isolate.

SRGIRIGPGRILAT 15

15

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, RF isolate.

15

MOLECULE TYPE: central region of the V3 loop from the gp120 protein of HIV-1, MN isolate.

15

**MOLECULE TYPE:** central region of the V3 loop from the gp120 protein of HIV-1, BRVA isolate

15

**MOLECULE TYPE:** central region of the V3 loop from the gp120 protein of HIV-1, IIIB isolate.

15

15

15

5

TAGGGASIRIQRGPGRFVTI 141

MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB9.

SEQUENCE IDENTIFICATION NO.: 20  
SEQUENCE TYPE: amino acid  
LENGTH: 202 amino acids  
MOLECULE TYPE: multiepitopic polypeptide (MEP) TAB13.

MVDKRMALVELKVPDIGGHENVDIHAVEVNVGDTIAVDDTLITLDLDSRGIRIGPGRAIL 60  
 ATAGGGAROSTPIGLGOALYTTAGGGARKSITKGPGRVIYATAGGGARKRIHIGPGRAFY 120  
 TTAGGGARKRITMGPRVYYTTAGGGARORTSIGOGOALYTTAGGGATSITIGPGOVFYR 180  
 TGAGGGASIRIQRGPGRAFVTI 202

SEQUENCE IDENTIFICATION NO.: 21  
SEQUENCE TYPE: Nucleotide  
LENGTH: 368 base pairs  
MOLECULE TYPE: Synthetic oligonucleotide  
PROPERTIES: Nucleotide fragment that codifies for the V3 epitopes bound by a AGGGA spacer in the MEP TAB9. Restriction sites XbaI (positions 1 to 6) and BamHI (positions 363 to 368) are introduced.

TCTAGACTCGAGAGGCATTTCGTATCGGGCCAGGTCGCGCAATTTTAGCAACAGCTGGCGG 60  
TGGCGCACGTCAATCTACCCCTATTGGTTTAGGTCAGGCTCTGTATACGACTGCCGGCGG 120  
TGGTGCGCGCAAAAGTATCACCAAGGGTCCAGGCCGCGTCATTTACGCCACCGCGGGCGG 180  
CGGTGCCCCGTAAGCGTATCCACATTGGCCCAGGCCGTGCATTCTATACTACAGCAGGTGG 240  
TGGCGCACGTAAACGCATCACTATGGGTCCTGGTCGCGTCTATTACACGACCGCTGGCGG 300  
CGGTGCTAGCATTTCGCATCCAACGCGGCCCTGGTCGTGCATTTGTGACCATATGATAACG 360  
CGGGATCC 368

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[illegible]

(C) E-MAIL: HMARZULLO@LSMAG.COM

(D) TOPOLOGY: Unknown

(B) STRAIN: B:4:P1.15

(B) CLONE: P64K

(D) OTHER INFORMATION: First 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp  
35 40 45

(A) LENGTH: 29 base pairs